

FIG. 1
(SEQ. ID NO: 1 & 2)

10	20	30	40	50	60	70	80	90
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
ATGCTTTGG	ACACAGCA	GTCACACAT	TATATATAG	AGGAATCA	AMGATGCC	ACTATGACT	ACAGTACATA	TGACTGATC
M A L E Q	N Q S T D	Y Y Y E	E N E M N G	T Y D Y	S Q Y E L I			
180								
TGATACAG	AGAGTTCAG	AGATTTGCA	AAATTTTCC	TGCTGINT	CTTCACATA	GTITTCGCA	TTCAGTCC	AGCAATTC
C I K E D	V R E F A	K V F L	P V F L	T I V F V I	G L A G N S			
270								
AGGATTCAG	CATTATTCAG	AAACAGGAA	CAAAACAGA	TGCTATCTC	CTGATTTGG	CTGTACGCA	TTCATCTCTT	
M V V A I	Y A Y Y K	K Q R T	K T D V	Y I L N L A	V A D L L L			
360								
CTATCATC	TGCTTTTGG	GGCTGTAT	GGAGTTCAG	GGTGGTTT	AGGGAATA	ATGTCAAAA	TACTTTCAGC	CTGTACACA
L F T L P	P W A V N	A V H G	W V L G	K I M C K I	T S A L Y T			
450								
CTAATTTG	TCTTCGAT	CGATTTCTG	GGTGTATCA	CGATGACAG	ATGTGTGCA	GTACTATAG	TGCTACGCA	ATCAGGATG
L N F V S	G M Q F L	A C I S	I D R Y	V A V T K V	P S Q S G V			
540								
GGAAACAT	CGTGTCTAT	CTGTTCCT	GTCTGATG	CTGCTGCT	CGTACGCTA	CGCTACCTG	TCTTTTATAC	AGTATATGAC
G K P C W	I I C F C	V W M A	A I L S I	P Q L V	F Y T V N D			
630								
ATGCTAGCT	CGATTCCT	TTTCTCTG	TTCTGCTA	CACTATGCA	AGCTATGAT	CAATCTGAT	AGATCTGAT	TGATTTCTA
N A R C I	P I F P R	Y L G T	S M K A	L I Q M L E	I C I G F V			
720								
GTCTCTTC	TCTATGCT	GGTGTCTC	TTTATCTAG	CAGCTACT	CATGAGATG	CGAATCTA	AAATCTCTG	ACCTCTTAA
V P F L I	M G V C Y	F I T A	R T L M K M	P N I K I	S R P L K			
810								
GTCTCTCA	CACTCTCT	AGTTTCTAT	GTCTCTAC	TGCTCTTA	CACTCTGAT	TCTCTGAT	CGATGATCT	CACTCTCTC
V L L T V	V I V F I	V T Q L	P Y N I	V K F C R A	I D I I Y S			
900								
CTCTCTCA	CTCTCTCT	CACTCTCT	ATCTCTCT	CGCTCTCT	ATCTCTCT	TCTCTCT	TCTCTCT	CTCTCTCT
L I T S C	N M S K R	M D I A	I Q V T E S	I A L F	H S C L N P			
990								
ATCTCTCT	TTTCTCTCT	AGCTCTCT	AACTCTCT	TCTCTCT	GGCTCTCT	TTCTCTCT	CGCTCTCT	CACTCTCT
I L Y V F	N G A S F	K N Y V	M K V A	K K Y G S W	R R Q R Q S			
1080								
GTCTCTCT	TTCTCTCT	TTCTCTCT	CTCTCTCT	CACTCTCT	TTCTCTCT	TCTCTCT	TTCTCTCT	CTCTCTCT
V E E F P	F D S E G	P T E P	T S T F S I	R N C S A	F C L			
1147								
GACTCTCT	ATCTCTCT	TGCTCTCT	TTCTCTCT	TTCTCTCT	TTCTCTCT	TTCTCTCT	TTCTCTCT	TTCTCTCT
D T Y E .	C F P L K	. N I C	L I L K K K	K K				

A

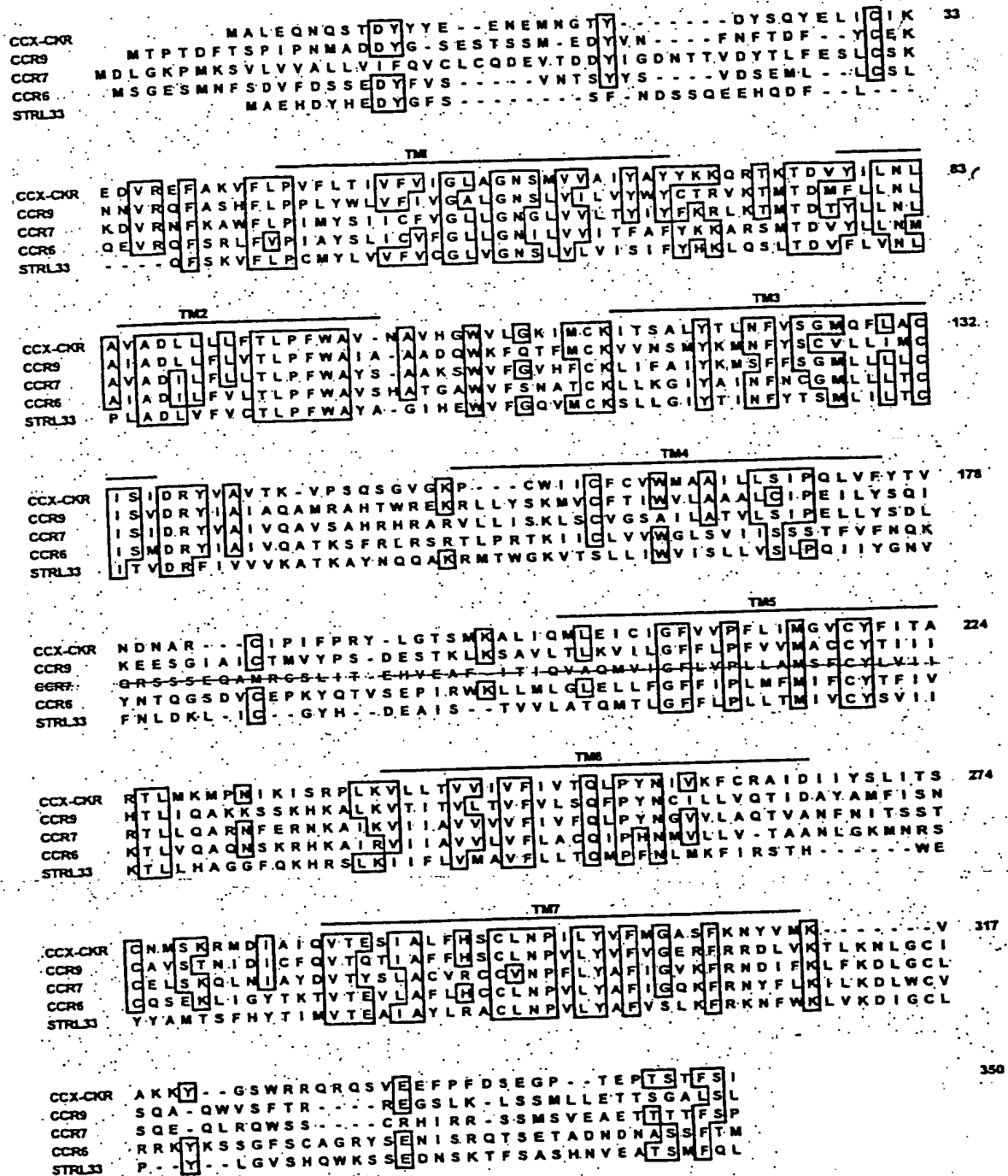


FIG. 2(a)

B

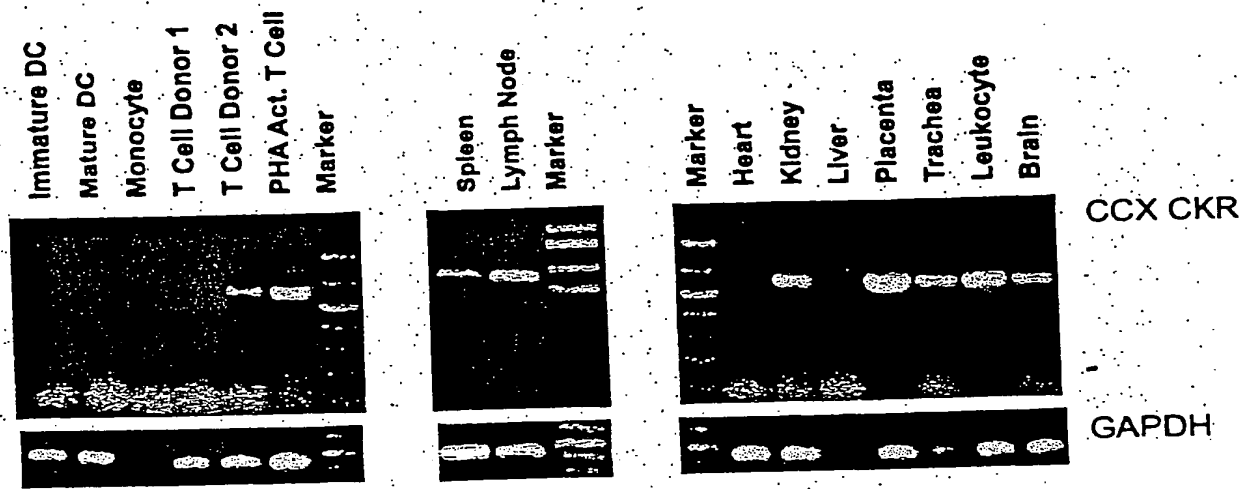


FIG. 2(b)

C

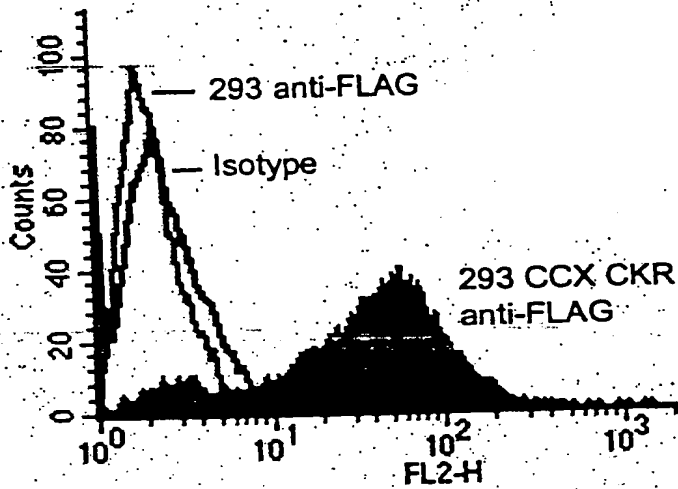
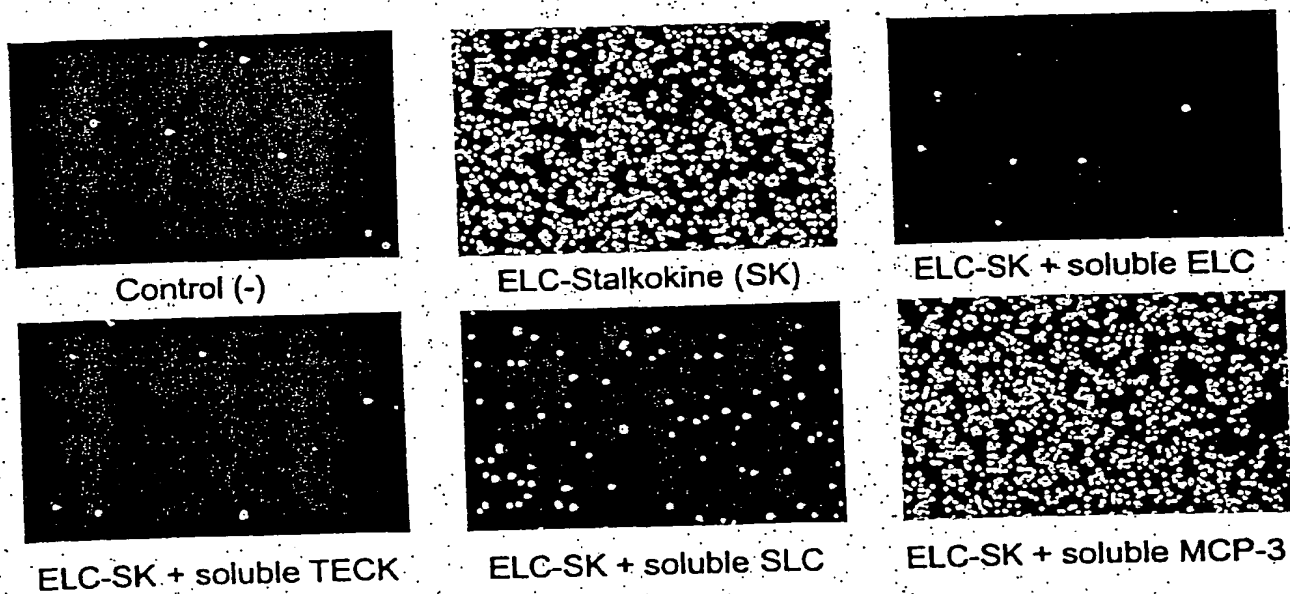


FIG. 2(c)

FIG. 3(a)



B

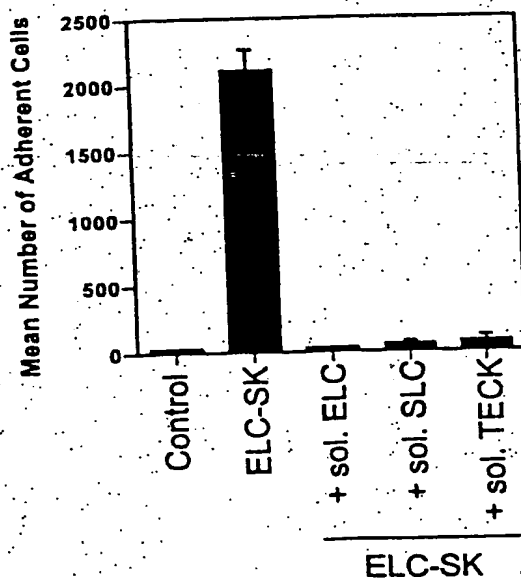


FIG. 3(b)

C

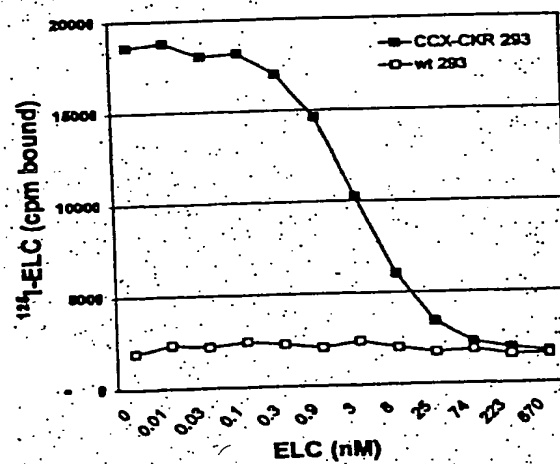


FIG. 3(c)

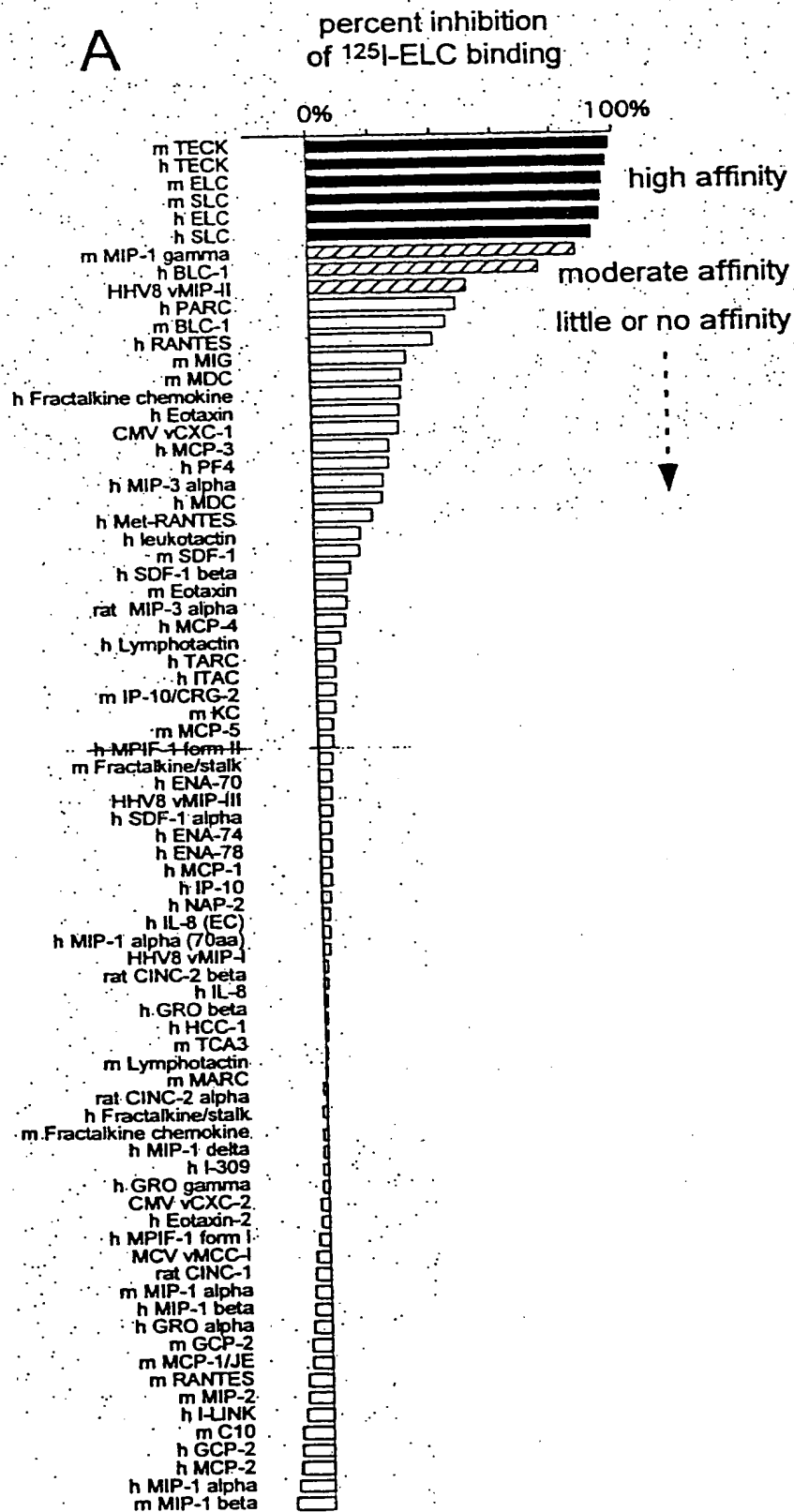


FIG. 4(a)

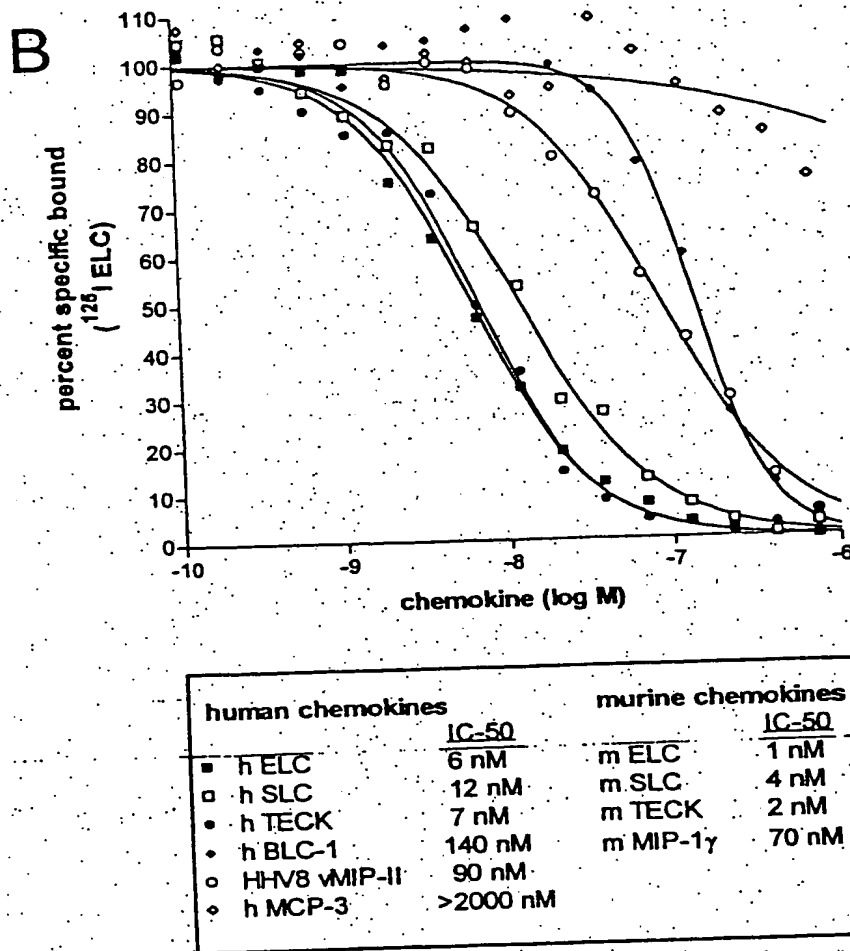


FIG. 4(b)

FIG. 5

5' upstream CCXCKR	ATGCAGCATC TGGTTTATAA AAGGCAACTA GTGAAATTTA GTGCAAATGC	50
5' upstream CCXCKR	TGAGAGAATT TATTTAACCTT ATTAAATTA AATTTATAAA TAACATCAAA	100
5' upstream CCXCKR	ATAAAAAATA AATTAAATTT AAATAAACCA AGTAATTGTC TATTTTCGTT	150
5' upstream CCXCKR	TTTATTCAAT TTGTGTAGA TATACTTTTA CGATTCACAA AATTATGTAT	200
5' upstream CCXCKR	GTAAGATTA TAACACTATT TATTCCTTTT AGTTAAATC TAATTAAATT	250
5' upstream CCXCKR	TTTATATTTT AAAAATCAAT TTACATAAA AGTCTTCACT TTTATTAGG	300
5' upstream CCXCKR	ATTAAATGAT TAAGAAAATT CTCCAGGGCA TTATGTTTAT TGTCTGTTC	350
5' upstream CCXCKR	AAATCCAAGC TCTTTCACAC AGAATTGTAC AAGCAAAGTT TGAGTAACTA	400
5' upstream CCXCKR	ATCTTGGGGT CATATTCCAA TGTGGCTCCC ATTAAAGCAT TTCAAAGAGT	450
5' upstream CCXCKR	GCTAGATTCA GGCCTACATA TGTTACAGCA ACAGGCTATA CTCTAGGGAA	500
5' upstream CCXCKR	AGAACAAAAC AGCTTGATAG AAAGTGTTG CTTTAAAGCA TATTTAGACA	550
5' upstream CCXCKR	AATATCTATC CTGTAATCTC TTGCCATCT AGATTGGAGC	600
5' upstream CCXCKR	translation start	9
5' upstream CCXCKR	649	58
5' upstream CCXCKR	685	108
5' upstream CCXCKR	734	147
5' upstream CCXCKR	740	197
5' upstream CCXCKR	740	247
5' upstream CCXCKR	740	297
5' upstream CCXCKR	740	347

Internalization by FACS 45 minute Incubation

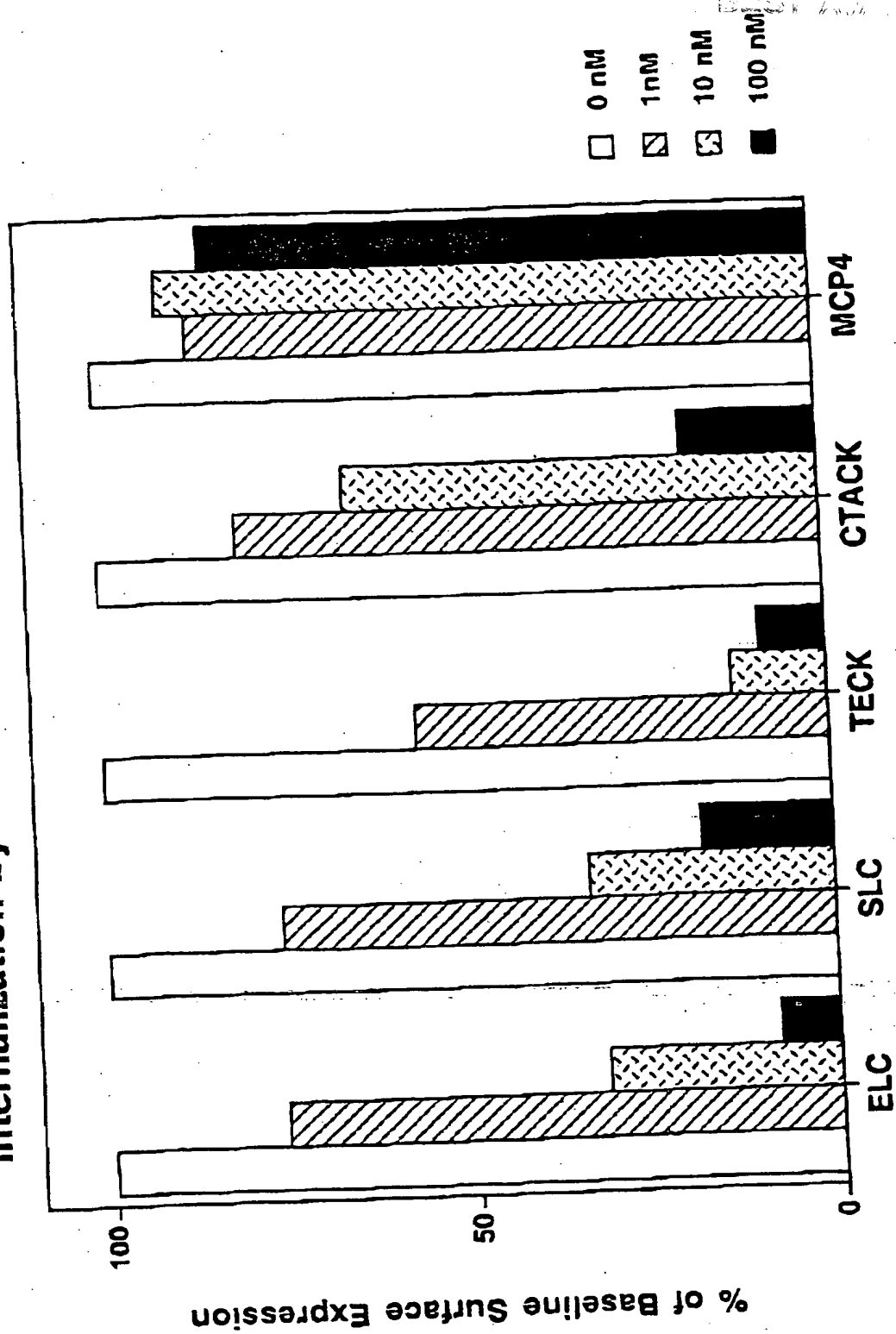


Fig. 6A

POST-TRANSLATIONAL MODIFICATION

Internalization by FACS 15 minute Incubation

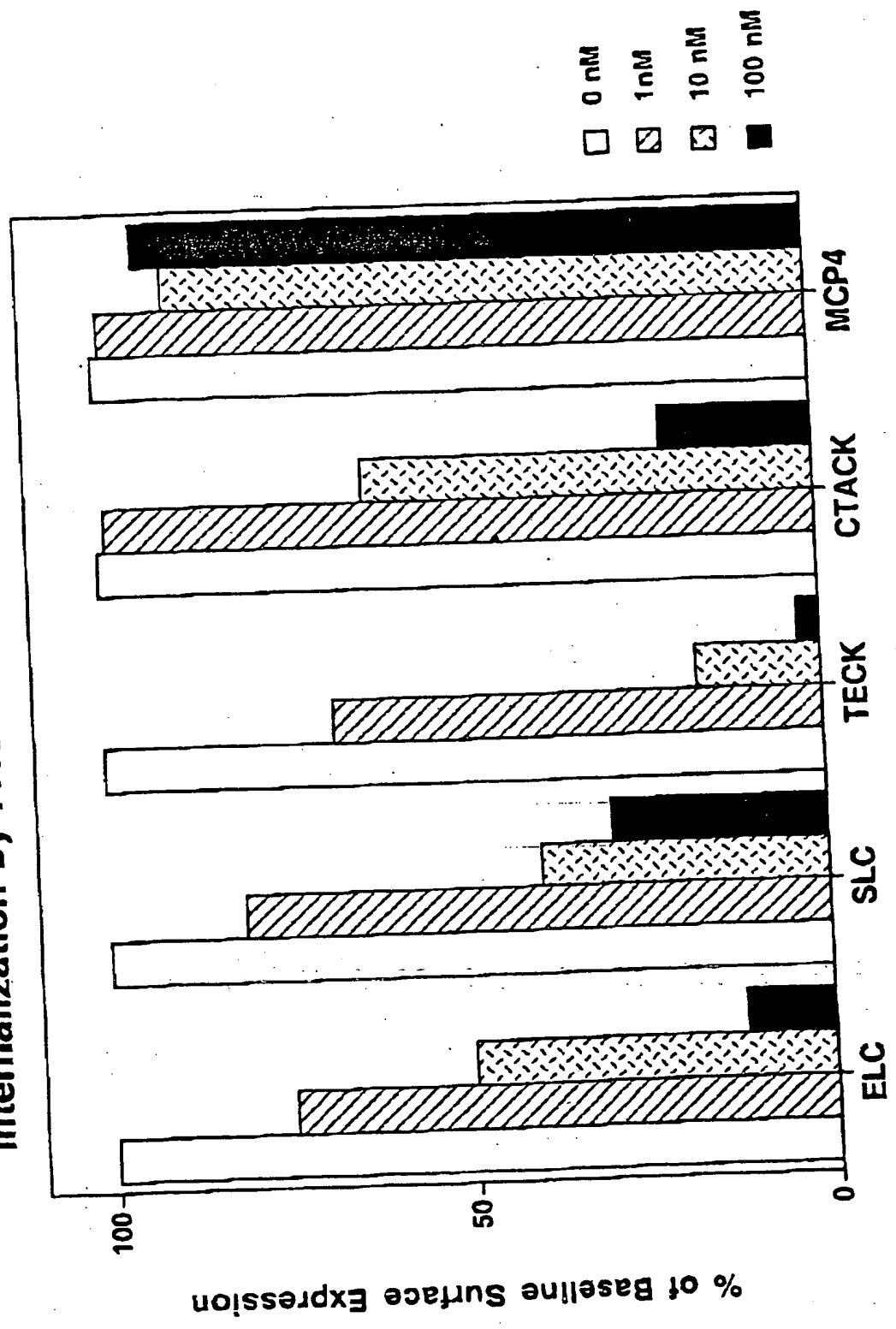


Fig. 6B